We claim:

1. An isolated polynucleotide consisting of a MNTF associated nucleic acid sequence selected from the group consisting of:

a) SEQ ID NO:1

b) a fragment of SEQ ID NO:1;

c) SEQ ID NO:2; and

d) a fragment of SEQ ID NO:2.

e) a nucleic acid sequence fully complementary to SEQ ID NO:1 or a fragment thereof.; and

f) a nucleic acid sequence fully complementary to SEQ ID NO:2 or a fragment thereof.

2. The isolated polynucleotide of claim 1, said fragment of SEQ ID NO:1 containing a 5' terminus selected from residues1-1849 of SEQ ID NO1, at least ten consecutive nucleic acid residues of SEQ ID NO:1 including the 5' terminus and a 3'terminus, wherein the 3' terminus is selected from residues 10-1859 of SEQ ID NO:1.

4. The isolated polynucleotide of claim 1, wherein the fragment of SEQ ID NO:1 is selected from the group consisting of:

a) SEQ ID NO:3;

b) SEQ ID NO:5;

c) SEQ ID NO:6; and

d) SEQ ID NO:10.

5. The isolated polynucleotide of claim 1 wherein the nucleic acid sequence fully complementary to a fragment of SEQ ID NO:1 is selected from the group consisting of:

a) SEQ ID NO:4;

b) SEQ ID NO:7;

c) SEQ ID NO:8;

d) SEQ ID NO:11; and

e) SEQ ID NO:12.

6. The isolated polynucleotide of claim 1, said fragment of SEQ ID NO;1 comprising at least one open reading frame.

7. The isolated polynucleotide of claim 6 wherein the at least one open reading frame encodes a polypeptide selected from the group consisting of:

a) SEQ ID NO:13;

b) SEQ ID NO:14;

c) SEQ ID NO:15;

d) SEQ ID NO:16;

e) SEQ ID NO:17;

f) SEQ ID NO:18;

g) SEQ ID NO:19;

h) SEQ ID NO:20;

i) SEQ ID NO:21;

a) SEQ ID NO:22;

b) SEQ ID NO:23;

c) SEQ ID NO:24;

d) SEQ ID NO:25;

e) SEQ ID NO:26;

f) SEQ ID NO:27;

g) SEQ ID NO:28;

h) SEQ ID NO:29;

i) SEQ ID NO:30;

j) SEQ ID NO 31; and

k) SEQ ID NO: 32.

8. A composition comprising a first polynucleotide and a second polynucleotide according to claim 7, wherein the first polynucleotide contains an open reading frame encoding SEQ ID NO:29.

9. The isolated polynucleotide of claim 1, said fragment of SEQ ID NO:2 comprising at least one putative MNTF promoter sequence and at least one open reading frame.

10. The isolated polynucleotide of claim 9 wherein said putative MNTF promoter sequence is selected from the group consisting of:

a) residues 862-911 of SEQ ID NO:2; and

b) residues 2315-2364 of SEQ ID NO:2.

11. The isolated polynucleotide of claim 10 wherein said fragment of SEQ ID NO:2 includes a potential transcription start sequence comprising residues 2501-4359 of SEQ ID NO:2.

12. The isolated polynucleotide of claim 9 wherein the at least one open reading frame encodes a polypeptide selected from the group consisting of:

a) SEQ ID NO:13;

b) SEQ ID NO:14;

c) SEQ ID NO:15;

d) SEQ ID NO:16;

e) SEQ ID NO:17;

f) SEQ ID NO:18;

g) SEQ ID NO:19;

h) SEQ ID NO:20;

i) SEQ ID NO:21;

j) SEQ ID NO:22;

k) SEQ ID NO:23;

l) SEQ ID NO:24;

m) SEQ ID NO:25;

n) SEQ ID NO:26;

o) SEQ ID NO:27;

p) SEQ ID NO:28;

q) SEQ ID NO:29;

r) SEQ ID NO:30;

s) SEQ ID NO 31; and

t) SEQ ID NO: 32.

13. An isolated MNTF associated polypeptide encoded by an open reading frame of SEQ ID NO:1.

14. A fusion protein comprising an MNTF associated polypeptide encoded by an open reading frame of SEQ ID NO:1 linked to a heterologous protein.

15. An expression vector operably linked to the isolated polynucleotide according to claim 1, wherein at least one open reading frame is operably linked to a control sequence compatible with a desired host vector.

16. An isolated host cell transformed with the expression vector of claim 15.

17. A method for determining the presence of a MNTF associated polynucleotide in a medium comprising the steps of:

contacting the medium, which may contain an MNTF associated nucleic acid sequence, with a synthesized and isolated oligonucleotide which under preselected hybridization conditions hybridizes with said MNTF associated nucleic acid sequence, but does not hybridize with nucleic acid sequences other than said MNTF associated nucleic acid sequence, in said medium; and

detecting, under said preselected hybridization conditions, the presence of said MNTF associated nucleic acid sequence.

18. A method of comparing the relative abundance of MNTF associated expression products in different samples comprising:

obtaining a first sample and a second sample, wherein the first sample differs from the second sample;

detecting a MNTF related expression product for the first sample and the second sample; and

comparing the relative abundance of the MNTF associated expression products of the first and second samples.

19. The method of claim 18, wherein MNTF RNA is the expression product.

20. The method of claim 18, wherein an MNTF associated polypeptide is the expression product.

22 The method of claim 18, wherein a polypeptide having at least SEQ ID No. 29 is the expression product.

23. The method of claim 18, wherein the comparison includes a step comprising hybridization with a nucleic acid probe complementary to the RNA.

23. A panel for use in hybridization assays comprising two or more polynucleotides according to claim 1 stably associated with the surface of a solid support.